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1648

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/744,176

DATE: 06/03/2002

TIME: 12:20:33

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\06032002\I744176.raw

mbH 3 <110> APPLICANT: Connex - Gesellschaft zur Optimierung von Forschung und Entwicklung

4 INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE (I.N.S.E.R.M.)

6 <120> TITLE OF INVENTION: Anti Hepatitis C virus antibody and uses thereof

8 <130> FILE REFERENCE: B3070PCT

C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/744,176

C--> 10 <141> CURRENT FILING DATE: 2001-06-18

10 <150> PRIOR APPLICATION NUMBER: EP 98 11 35 95.7

11 <151> PRIOR FILING DATE: 1998-07-21

13 <160> NUMBER OF SEQ ID NOS: 6

15 <170> SOFTWARE: PatentIn Ver. 2.1

17 <210> SEQ ID NO: 1

18 <211> LENGTH: 324

19 <212> TYPE: DNA

20 <213> ORGANISM: Homo sapiens

22 <220> FEATURE:

23 <221> NAME/KEY: CDS

24 <222> LOCATION: (1)..(324)

26 <400> SEQUENCE: 1

| | | |
|----|---|-----|
| 27 | tct tac gag ctc acg cag ccg ccc tcg gtg tca gtg tcc cca gga cag | 48 |
| 28 | Ser Tyr Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ser Pro Gly Gln | |
| 29 | 1 5 10 15 | |
| 31 | acg gcc agg atc acc tgc tct gga gat gca ttg cca aag caa tat gct | 96 |
| 32 | Thr Ala Arg Ile Thr Cys Ser Gly Asp Ala Leu Pro Lys Gln Tyr Ala | |
| 33 | 20 25 30 | |
| 35 | tac tgg tat cag cag aag cca ggc cag gcc cct gtg ttg gtg ata tat | 144 |
| 36 | Tyr Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr | |
| 37 | 35 40 45 | |
| 39 | aaa gat aat gag agg ccc tca ggg atc cct gag cga ttc tct ggc tcc | 192 |
| 40 | Lys Asp Asn Glu Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser | |
| 41 | 50 55 60 | |
| 43 | agg tca ggg aca aca gtc acg ttg acc atc agt gga gtc cag gca gaa | 240 |
| 44 | Arg Ser Gly Thr Thr Val Thr Leu Thr Ile Ser Gly Val Gln Ala Glu | |
| 45 | 65 70 75 80 | |
| 47 | gac gag gct gac tat tac tgt caa tca gca gac agc agt ggt tct tcc | 288 |
| 48 | Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Ala Asp Ser Ser Gly Ser Ser | |
| 49 | 85 90 95 | |
| 51 | tgg gtg ttc ggc gga ggg acc aag ctg acc gtc cta | 324 |
| 52 | Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu | |
| 53 | 100 105 | |
| 56 | <210> SEQ ID NO: 2 | |
| 57 | <211> LENGTH: 108 | |
| 58 | <212> TYPE: PRT | |
| 59 | <213> ORGANISM: Homo sapiens | |

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61 <400> SEQUENCE: 2

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62 Ser Tyr Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ser Pro Gly Gln
63   1           5           10           15
65 Thr Ala Arg Ile Thr Cys Ser Gly Asp Ala Leu Pro Lys Gln Tyr Ala
66           20           25           30
68 Tyr Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
69           35           40           45
71 Lys Asp Asn Glu Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
72   50           55           60
74 Arg Ser Gly Thr Thr Val Thr Leu Thr Ile Ser Gly Val Gln Ala Glu
75 65           70           75           80
77 Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Ala Asp Ser Ser Gly Ser Ser
78           85           90           95
80 Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
81           100          105

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85 <210> SEQ ID NO: 3

86 <211> LENGTH: 351

87 <212> TYPE: DNA

88 <213> ORGANISM: Homo sapiens

90 <220> FEATURE:

91 <221> NAME/KEY: CDS

92 <222> LOCATION: (1)..(351)

94 <400> SEQUENCE: 3

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95 cag gtg cag cta cag cag tgg ggc gca gga ctg ttg aag cct tcg gag      48
96 Gln Val Gln Leu Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Ser Glu
97   1           5           10           15
99 acc ctg tcc ctc acc tgc gct gtc tat ggt ggg tcc tta agt ggt tac      96
100 Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Leu Ser Gly Tyr
101           20           25           30
103 ttc tgg acc tgg atc cgc cag tcc ccc ggg aag ggg ctg gag tgg att     144
104 Phe Trp Thr Trp Ile Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Ile
105           35           40           45
107 ggg gaa agc aat tat agt gga agt acc agg tac aac ccg tcc ctc aag     192
108 Gly Glu Ser Asn Tyr Ser Gly Ser Thr Arg Tyr Asn Pro Ser Leu Lys
109           50           55           60
111 agt cga gtc acc ata tca gta gac acg tcc cag aac cag ttc tcc ctg     240
112 Ser Arg Val Thr Ile Ser Val Asp Thr Ser Gln Asn Gln Phe Ser Leu
113 65           70           75           80
115 aag ctg agc tct gtg acc gcc gcg gac acg gct gta tat tac tgt gcg     288
116 Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
117           85           90           95
119 aga ggt tgg gcg gtg gac ggt atg gac gtc tgg ggc caa ggg acc acg     336
120 Arg Gly Trp Ala Val Asp Gly Met Asp Val Trp Gly Gln Gly Thr Thr
121           100          105          110
123 gtc acc gtc tcc tca                                             351
124 Val Thr Val Ser Ser
125           115
128 <210> SEQ ID NO: 4
129 <211> LENGTH: 117

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130 <212> TYPE: PRT
131 <213> ORGANISM: Homo sapiens
133 <400> SEQUENCE: 4
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135 1 5 10 15
137 Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Leu Ser Gly Tyr
138 20 25 30
140 Phe Trp Thr Trp Ile Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Ile
141 35 40 45
143 Gly Glu Ser Asn Tyr Ser Gly Ser Thr Arg Tyr Asn Pro Ser Leu Lys
144 50 55 60
146 Ser Arg Val Thr Ile Ser Val Asp Thr Ser Gln Asn Gln Phe Ser Leu
147 65 70 75 80
149 Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
150 85 90 95
152 Arg Gly Trp Ala Val Asp Gly Met Asp Val Trp Gly Gln Gly Thr Thr
153 100 105 110
155 Val Thr Val Ser Ser
156 115
160 <210> SEQ ID NO: 5
161 <211> LENGTH: 324
162 <212> TYPE: DNA
163 <213> ORGANISM: Homo sapiens
165 <220> FEATURE:
166 <221> NAME/KEY: CDS
167 <222> LOCATION: (1)..(324)
169 <400> SEQUENCE: 5
170 tcc tct gag ctg aca cag cca ccc tcg gtg tca gtg tcc cca gga cag 48
171 Ser Ser Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ser Pro Gly Gln
172 1 5 10 15
174 acg gcc agg atc acc tgc tct gga gat gca ttg cca aag caa tat gct 96
175 Thr Ala Arg Ile Thr Cys Ser Gly Asp Ala Leu Pro Lys Gln Tyr Ala
176 20 25 30
178 tac tgg tat cag cag aag cca ggc cag gcc cct gtg ttg gtg ata tat 144
179 Tyr Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
180 35 40 45
182 aaa gat aat gag agg ccc tca ggg atc cct gag cga ttc tct ggc tcc 192
183 Lys Asp Asn Glu Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
184 50 55 60
186 agg tca ggg aca aca gtc acg ttg acc atc agt gga gtc cag gca gaa 240
187 Arg Ser Gly Thr Thr Val Thr Leu Thr Ile Ser Gly Val Gln Ala Glu
188 65 70 75 80
190 gac gag gct gac tat tgt caa tca gca gac agc agt ggt tct tcc 288
191 Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Ala Asp Ser Ser Gly Ser Ser
192 85 90 95
194 tgg gtg ttc ggc gga ggg acc aag ctg acc gtc cta 324
195 Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
196 100 105
199 <210> SEQ ID NO: 6

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200 <211> LENGTH: 108
201 <212> TYPE: PRT
202 <213> ORGANISM: Homo sapiens
204 <400> SEQUENCE: 6
205 Ser Ser Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ser Pro Gly Gln
206   1           5           10           15
208 Thr Ala Arg Ile Thr Cys Ser Gly Asp Ala Leu Pro Lys Gln Tyr Ala
209           20           25           30
211 Tyr Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
212           35           40           45
214 Lys Asp Asn Glu Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
215           50           55           60
217 Arg Ser Gly Thr Thr Val Thr Leu Thr Ile Ser Gly Val Gln Ala Glu
218   65           70           75           80
220 Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Ala Asp Ser Ser Gly Ser Ser
221           85           90           95
223 Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
224           100          105

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VERIFICATION SUMMARY

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L:10 M:270 C: Current Application Number differs, Replaced Current Application No

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date